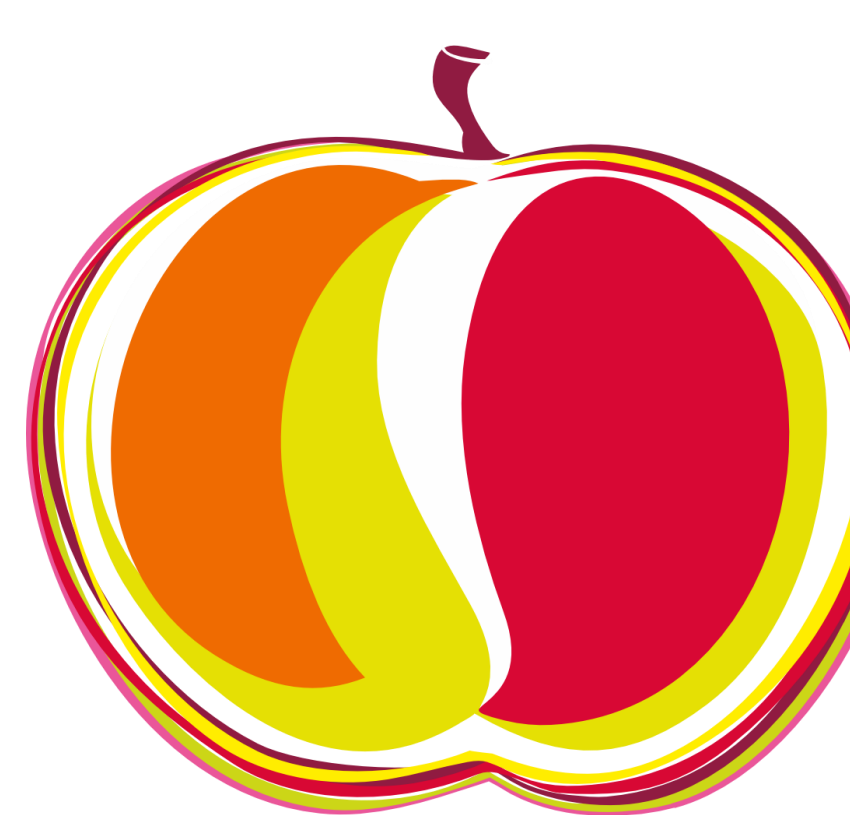




FruitBreedomics

BRIDGING THE GAP BETWEEN GENOMICS
AND FRUIT BREEDING



ISTITUTO AGRARIO DI SAN MICHELE ALL'ADIGE
Fondazione Edmund Mach

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A second generation peach linkage map using the IPSC 9K SNP chip for advanced QTL identificaion

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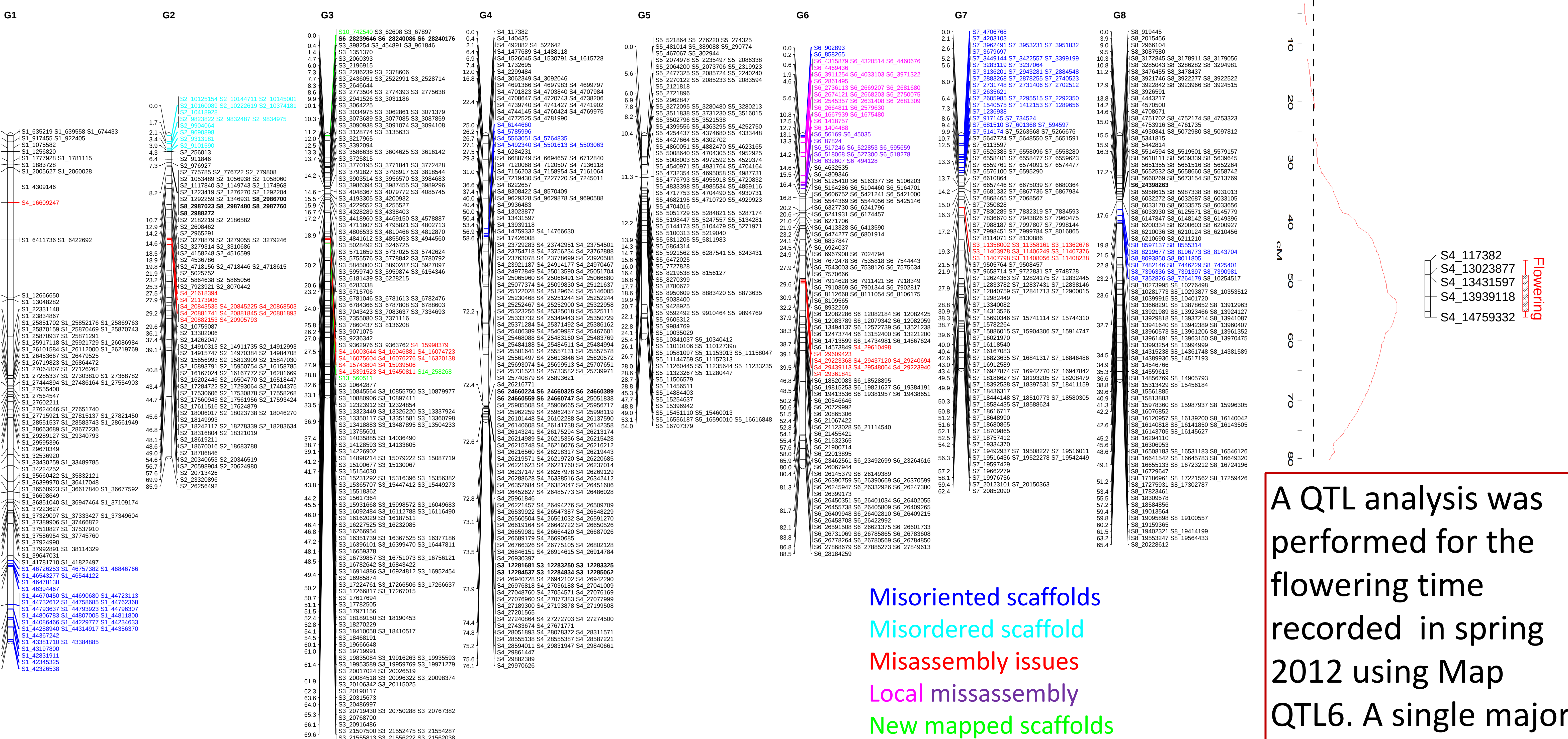
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Context

Peach [*Prunus persica* (L.) Batsch] is one of the most important fruit crops in temperate area. Peach breeding is costly and time consuming due to the size of the plants and the relatively long (3-4 years) intergeneration period. Marker assisted breeding can help in reducing the cost and time in obtaining improved cultivars. The availability of the complete peach genome sequence (International Peach Genome Initiative, IPGI) allowed the development of a powerful genetic tool, a 9K SNP chip delivered by the International Peach SNP Consortium, IPSC. The chip is being employed within the EU funded project FruitBreedomics to dissect QTL and identify SNPs linked to important agricultural traits.

Results



SNPs were named according to their position on Peach v1.0 pseudomolecules

Markers in bold represent putative duplicated loci

The linkage map was obtained with Joinmap 4.1 using 1314 SNPs of the IPSC 9K chip using 232 individuals of the BC1 progeny of PXF (*P.persica* X *P.ferganensis*) population. The map is distributed in 8 linkage group and covers 637.3 cM with an average distance of 0.5 cM. The map aligns completely with the eight peach v1.0 pseudomolecules (IPGI). The observed discrepancies highlighted few misassembly and orientation issues (see the legenda). The genetic by physical distance ratio is on average 325 kb per cM.